```
                 GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:    December 6, 2002, 21:11:51 ; Search time 45 Seconds
                                   (without alignments)
                              10392.935 Million cell updates/sec

Title:         US-10-025-514-7
Perfect score: 1525
Sequence:      1 tctagaccatgtctggaaag.........ccaactcagaagtagtcgac 1525

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued_Patents_NA:*
            1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
            2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
            3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
            4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
            5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
            6: /cgn2_6/ptodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	630.4	41.3	1308	3	US-09-023-173-10	Sequence 10, Appl
2	630.4	41.3	1308	3	US-09-023-339-6	Sequence 6, Appl
3	629.4	41.3	1185	3	US-09-023-339-3	Sequence 3, Appl
4	629.4	41.3	1260	3	US-09-299-141-4	Sequence 4, Appl
5	433.2	28.4	5932	4	US-09-299-141-4	Sequence 4, Appl
6	433.2	28.4	6142	4	US-09-299-141-8	Sequence 8, Appl
7	433.2	28.4	6565	4	US-09-299-141-1	Sequence 1, Appl
8	433.2	28.4	6714	4	US-09-299-141-6	Sequence 6, Appl
9	433.2	28.4	6924	4	US-09-299-141-9	Sequence 9, Appl
10	433.2	28.4	6924	4	US-09-299-141-10	Sequence 10, Appl
11	433.2	28.4	6924	4	US-09-299-141-11	Sequence 11, Appl
12	433.2	28.4	6981	4	US-09-299-141-7	Sequence 7, Appl
13	433.2	28.4	7054	4	US-09-299-141-3	Sequence 3, Appl
14	430.4	28.4	7405	4	US-09-299-141-2	Sequence 2, Appl
15	428.2	28.2	1185	3	US-09-023-339-2	Sequence 2, Appl
16	408.8	26.8	1356	1	US-08-002-202-16	Sequence 16, Appl
17	408.8	26.8	1356	1	US-08-481-534-16	Sequence 16, Appl
18	407.2	26.7	1356	1	US-08-002-202-12	Sequence 12, Appl
19	407.2	26.7	1356	3	US-08-481-534-12	Sequence 12, Appl
20	404	26.5	1356	1	US-08-002-202-18	Sequence 18, Appl
21	404	26.5	1356	1	US-08-481-534-18	Sequence 18, Appl
22	313.2	20.5	1339	1	US-07-859-480-1	Sequence 1, Appl
23	228.6	15.0	7492	4	US-09-299-141-5	Sequence 5, Appl
24	219.2	14.4	1423	1	US-07-829-954-1	Sequence 1, Appl
25	219.2	14.4	1423	1	US-07-994-423-1	Sequence 1, Appl
26	219.2	14.4	1423	1	US-08-421-891-1	Sequence 1, Appl
27	210.6	13.8	10627	1	US-08-060-925A-12	Sequence 12, Appl

				ID	Description
28	124.6	8.2	2466	4	US-09-271-608-7	Sequence 7, Appl
29	124.6	8.2	2466	4	US-09-695-950-7	Sequence 7, Appl
30	124.6	8.2	2466	4	US-09-696-147-7	Sequence 7, Appl
31	124.6	8.2	2466	4	US-09-696-364-7	Sequence 7, Appl
32	123.2	8.1	194	2	US-07-963-538B-5	Sequence 5, Appl
33	123	8.1	180	3	US-08-483-503A-2	Sequence 2, Appl
34	106.4	7.0	1508	3	US-08-660-347-1	Sequence 1, Appl
35	81.6	5.4	1179	4	US-08-745-995A-22	Sequence 22, Appl
36	81.6	5.4	1179	4	US-08-745-995A-23	Sequence 23, Appl
37	81.6	5.4	1191	4	US-08-745-995A-4	Sequence 4, Appl
38	81.6	5.4	1191	4	US-08-745-995A-5	Sequence 5, Appl
39	81.6	5.4	1191	4	US-08-745-995A-34	Sequence 35, Appl
40	81.6	5.4	1191	4	US-08-745-995A-35	Sequence 35, Appl
41	81.6	5.4	1197	4	US-08-745-995A-10	Sequence 10, Appl
42	81.6	5.4	1197	4	US-08-745-995A-11	Sequence 11, Appl
43	81.6	5.4	1191	4	US-08-745-995A-16	Sequence 16, Appl
44	81.6	5.4	1260	4	US-08-745-995A-17	Sequence 17, Appl
45	81.6	5.4	1358	4	US-08-745-995A-7	Sequence 7, Appl

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                        ALIGNMENTS

RESULT 1
US-09-023-173-10
; Sequence 10, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
;   APPLICANT: Sutliff, Thomas D.
;   APPLICANT: Rodriguez, Raymond L.
;   TITLE OF INVENTION: Production of Mature Proteins
;   TITLE OF INVENTION: in Plants
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Dehlinger & Associates
;     STREET: 350 Cambridge Ave., Suite 250
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/023,173
;     FILING DATE: 13-FEB-1998
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/038,168
;     FILING DATE: 13-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Petithory, Joanne R
;     REGISTRATION NUMBER: P42995
;     REFERENCE/DOCKET NUMBER: 0665-0007.30
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-324-0880
;     TELEFAX: 650-324-0960
;   INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1308 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-09-023-173-10

Query Match             41.3%;  Score 630.4;  DB 3;  Length 1308;
Best Local Similarity   70.8%;           Pred. No. 1.3e-153;
  Matches  838;  Conservative  0;  Mismatches 346;  Indels  0;  Gaps  0;

Qy   335 GGAAGACCCTCAAGGCGACGGCGCGCTCAAAAAACCGACACCAGTCATCACGACGACCAACCAAGACCA 394
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```
Db   116  GGAGGACCCGCAGGCGACGCCGCCCAGAAGACCGGACACCCAGCAGCCAGCAGACCA   175
          ||||| | |||| |||||||||| | ||||||| || ||| |   |  |  |
Qy   395  TCCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTTATAGACA  454

Db   176  CCCGACGTTCAACAAGATCACCCCGAATTGGCCGAATTCGCCTTCAGCCTGTACCGCCA   235
          ||||| ||| || |  |  |  |  |  |  |  |   |   |  |     | |
Qy   455  ATTAGCTCATCAAAGTAATTCTACTAAACATTTTTTTTGTCGTTGTTCTATTGCCACTGC  514

Db   236  GCTCCGCGCACCAGTCCAACTCCACCAACATCTTCTTCAGCCCGTGAGCATCGCCACCGC  295
          ||||||| | | ||| || || || || ||| ||  ||   ||  | | | ||||||||
Qy   515  TTTCCCCATGTGTGAGTTTAGGTACTAAAGCCGATACCCATGCATGGATTTTAGAAGGTTT  574

Db   296  CTTCGGCCATGCTGTCCCGGGTACCCAGGTTTTCAAGAGTTGTT                 355
          || |||| | | || || ||||| | |||||| ||||| |||||
Qy   575  AAACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGTTTTCAAGAGTTGTT   634

Db   356  GAACTTCAACCTGACCGAGATCCCGAGGCCCAGATCCACGAGGGCCTTCCAGAGCTGCT   415
          |||| ||  |||   |  || ||| || |||||||||||| || | | || ||| ||
Qy   635  GAGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGTAACGGTTTATTTTT   694

Db   416  CAGGACGCTCAACCAGCCGGACTCCCAGCTCCAGCTCACCACCGCAACGGCGTCTTCCT   475
          ||||| | |  | ||| || || || |||||||||| || | | || ||||| ||||
Qy   695  GCTCGAAGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAG   754

Db   476  GTCCCGAGGGCCTCAACTGCTCGTCAACTACGATAAGTTCCTGGAGGACGTCTACCACTC   535
          |  |||||| | |   ||| |  || ||  |   |  | ||| || || | | ||||||
Qy   755  TGAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGCTAAAAGCAAATTAATGATTA   814

Db   536  CGAGGCGTTCACCGTCAACTTCGGGGACACCGAGAAGCAGAGGCCAGATCAACGACTA   595
          ||||||| || | ||| ||  |  || ||   | || || || | |  |  ||| | |
Qy   815  TGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATAC   874

Db   596  CGTCAGAAGGGGACCCAGGGACCAAGATCGTGTCAAGGATTGGACAGGGACAC        655
          |  | || ||||  || ||| ||| || ||  |  |  | || || ||| |||
Qy   875  CGTCTTCGCCACTAGTTAACTATATTTTTTTCAAGGGTAAGTGGGAACGTCCTTCGAGGT  934

Db   656  CGTCTTCGGCGGCTCGTCAACTACATCTTCTTCAAGGGCAAGTGGAGCGCCCGTTCGAGGT  715
          ||||||||| |||||||||| || |||||||| || || ||||||| | || ||||||||
Qy   935  TAAAGATACTGAAGAGGAAGAGATTTCATGTGATCAAGTTGATCAAAAGTTCCTCCAAT  994

Db   716  GAAGGACACCGAGGAGGAGGAGCTTCCACGGTCACCACGTCAAGGTCCAAGGTCCTTGGGTCTT  1054 (continued)
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Qy   995  GATGAAAGACTGGGTATGTTCAATATTCAAATTCAACACTGCACTGATAAAATTAAGTTCTTGGGTCTT  1054
Db   776  GATGAAGAGGAGCTCGGCATGTTCAACATCAACACTGCACTCAAGAAGCTCTCCAGCTGGGTGCT      835

Qy  1055  ATTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTTTTTTTTTTTTACCAGACGAAGGTAAGCT  1114
Db   836  CCTCATGAAGTACCTGGGGAACGCCACGGCGGCCACCGCCATCTTCTTCCTGCCGGACGAGGGCAAGCT  895

Qy  1115  TCAACATTTAGAGAATGAGTTGACTCATGACGTATTATTCATGACATATTATTACTAAATTTTTAGAGAACGAGGA  1174
Db   896  CCAGCACCTGGAGAACGAGCTGACGCACGATCATCACGAAGTTCCTGGAGACGAGGA       955

Qy  1175  TCGTTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAA  1234
Db   956  CAGGCGCTCCGCTAGCCTCACCTCCACCTCCACCTCCACCGCACGTGCCGATTTGAGTGG  1015

Qy  1235  ATCTGTTTTAGGCCAGTTAGTTATTACCAAAAGTTTTTTTCTTAACGGTGCCGATTTGAGTGG  1294
Db  1016  GAGCGTGCTGGCCAGCTGGGCATCACGAAGGTCTTCAGCAACGGCGGGACCTCTCCGG      1075

Qy  1295  TGTTACTGAAGAAGCTGGGTATGTTCAATTTTGAGTAAAAGCCGTCTTCACAAAGCCGTCTAAACTAT  1354
Db  1076  CGTGACGGAGGAGCCCCCGCCCCTGAAGCTCTCCAAGGCCGTGCTGCACAGGCGGTGCTCACGAT     1135

Qy  1355  TGATGAAAAGGGTACCGAGGCGCGCGTCGGGGCGCTATTGTTCCTGGAAGCTATTCCCAATGAGCAT  1414
Db  1136  CGACAGAAGGGGACGGAAGCTGCCGGGGCCGCTGCTGCCCATGGCCATCCCCATGTCCAT      1195

Qy  1415  TCCACCAGAAGTGTCAAGTTCAACAAGACCCCTTCGTCTTCGTCCTTCGATGATCGAGCAGAACACTAA  1474
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Qy  1475  AAGCCCATTCTTTATGGTGGTAAGGTTGTCAACCCAACTCAGAAGT  1518
          ||||| ||| |||||| |||||||| ||| |||||| ||||||||||
Db  1256  GAGCCCCCTCTTCATGGGAAGGTCGTCAACCCCACGCAGAAGT     1299
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RESULT 2
US-09-023-339-6
; Sequence 6, Application US/09023339
; Patent No. 6127145
GENERAL INFORMATION:
APPLICANT: Sutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of '1-Antitrypsin
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,339
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: codon-optimized No. 6127145I/XhoI fragment encoding RAmy3D
CLONE: signal peptide-AAT fusion protein
US-09-023-339-6

Query Match   41.3%; Score 630.4; DB 3; Length 1308;
Best Local Similarity   70.8%; Pred. No. 1.3e-153;
Matches 838; Conservative   0; Mismatches 346; Indels   0; Gaps   0;

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Qy   335  GGAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCA  394
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Db   116  GGAGGACCCGCAGGCGACGCCGCCCAGAAGACCGACACCAGCAGCCAGCAGACCAAGACCA  175

Qy   395  TCCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTTATAGACA  454
          ||||| ||| || |  |  || ||  |  |  ||||||| ||  || ||  |||| | | |
Db   116  CCCGACGTTCAACAAGATCACCCCGAATTGGCCGAATTCGCCTTCAGCCTGTACCGCCA   175

Qy   395  TCCGACTTTTAATAAAATTACTCCAAATTTACTCCAAATTTTCTTTGTTATAGACA  454
          |||| || |  |  | || || |  |  |  || | |||| |  || ||||||||||
Db   176  CCCGACGTTCAACAAGATCACCCCGGGTACCCTGGGTACCGCCA           235

Qy   455  ATTAGCTCATCAAAGTAATTCTACTAAACATTTTTTTTTGTCGTTGTTCTATTGCCACTGC  514
          | |||||||||||| |  | | | |  |  | || |  | |  |  |   | |||| || | ||
Db   236  GCTCCGCGCACCAGTCCAACTCCACCAACATCTTCTTCAGCCCGTGAGCATCGCCACCGC  295

Qy   515  TTTCCCCATGTGTGAGTTTAGGTACTAAAGCCGATACCCATGCATGGATTTTAGAAGGTTT  574
          ||| |||| | | ||  || |  ||| ||  || | | ||   || | | | |||| |||||
Db   296  CTTCGGCCATGCTGTCCCGGGTACCCAGGTTTTCAAGAGTTGTTCAAGAGTTGTT       355

Qy   575  AAACTTTAATTTGACCGAAATCCCAGAAATCCCAGAAGCCCAAATTCACGAGGTTTTCAAGAGTTGTT  634
          ||| || |  ||  |  || |||||| || |  | |||| || | ||||||||||||||||||||||||
Db   296  CTTCGGCCATGCTGTCCCGGGTACCCGGGTACCGCCACCAGGGCCATCGCCACCGC                 295
```

```
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Dehlinger & Associates
   STREET: P.O. Box 60850
   CITY: Palo Alto
   STATE: CA
   COUNTRY: USA
   ZIP: 94306
COMPUTER READABLE FORM:
   MEDIUM TYPE: Diskette
   COMPUTER: IBM Compatible
   OPERATING SYSTEM: DOS
   SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/023,339
   FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 60/037,991
   FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
   NAME: Petlchory, Joanne R
   REGISTRATION NUMBER: P42,995
   REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 650-324-0880
   TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:     3:
SEQUENCE CHARACTERISTICS:
   LENGTH: 1185 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
IMMEDIATE SOURCE:
   CLONE: codon-optimized AAT coding sequence
US-09-023-339-3

Query Match             41.3%;  Score 629.4;  DB 3;  Length 1185;
Best Local Similarity   70.8%;  Pred. No. 2.2e-153;
Matches  837;  Conservative    0;  Mismatches  346;  Indels    0;  Gaps    0;

Qy    336 GAAGACCCTCAAGGCGACGCGCCCTCAAAAACCGACACCAGTCATCACGACCAGACCAT 395
          || |||||| || |||||||| ||||| || |||||||||||||| |||||||||||
Db      1 GAGGACCCGCAGGCGGCGCCGCCCCAGAAGACCGACACCAGCCACCAGACCAGGACCAC 60

Qy    396 CCGACTTTTAATAAAATTACTCCAAATTTAGGCGGAGAACGTCAAGAAACTATATCATAG 455
          ||||| || ||| || || || ||||| |||| || |||||| ||| ||| || |
Db     61 CCGACGTTCAACAAGATCACCCCGAATTTGGCGCGTGAGAATTGGCGGCAAGCTCTACTAT 120

Qy    456 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTTAGTCGTGTTTGTTCTATTGCCACTGCT 515
          | |||| | ||||| | ||||  | ||| ||| || || |||| |||||| |||||
Db    121 CTCGGCGACCAGTCAACTCCACCAACATCTTCTTCAGCCCGGTTGAGCATCGCCACCGCC 180

Qy    516 TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATTGCAATTACTGTAACTACTGTTTA 575
          ||||||  || || |||| || |||||||||| |||||| || ||||| || ||||||
Db    181 TTCGCCATGTTGTCCCTGGGTACCAAGCGGCACACCCACGACACCAGATCCGAAGGGCTG 240

Qy    576 AACTTTAATTGACCAGAATCCAGAGAAGCCCAAATTCACGAGGGTTTCACGAGTTGTTG 635
          ||||| || ||| ||| || || ||||| |||||| || |||| ||| ||||| |
Db    241 AACTTCAACCTGACGGAGATCCCGGAGGGCCAGATCCCAGGAGCTCCAGAGGTGCTC 300

Qy    636 AGAACTTTGAATCAACCTGCTCCAGTTCAATTGCAATTAACTACTGTAACGGTCTTATTTTTG 695
          |||| || || ||| ||| |||||| |||| ||||| | |||||| || || ||| |
Db    301 AGGACGCTCAACGCCCGGCTCCAGCTCCCAGCTCCACCACCTCCACCTCCACCTCCTG 360

Qy    696 TCTGAAGGTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 755
          ||| || ||||| || || ||| || || || ||| || || ||| || || || |
Db    361 TCCGAGGGCCTCAAGCTCCGATAAGTTCCTGGAGACGTGAAGAAGCTTCACCACTCC 420

Qy    756 GAGGCTTTTACCGTTAATTTGGTGATACTGAGGAGTAAAAAGCAAATTAATGATTAT 815
          |||||  ||| ||| ||||| || || |||| || || |||| ||| || ||||| ||
Db    421 GAGGCGTTCACCGTCAACTTCGGGGACACCGAGGGCGAAGAAGCCAAGAAGAGATCAACGACTAC 480

Qy    816 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 875
          ||||| ||||||||||| |||| || || || ||| |||| || ||| || |||||||
Db    481 GAGGCGTTCACCGTCAACTTCGGGGACACCGAGGGCGAAGAAGCCAAGAAGAGATCAACGACTAC 
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Db    356 CTGCT 415
Qy    635 TATTTT 694
Db    416 CTTCCT 475
Qy    695 CATATAG 754
Db    476 CCACTC 535
Qy    755 AATGATTA 814
Db    536 AACGACTA 595
Qy    815 CGTGATAC 874
Db    596 AGGACAC 655
Qy    875 TTCCAGGT 934
Db    656 TTCGAGGT 715
Qy    935 GTCCAAT 994
Db    716 CCCGAT 775
Qy    995 TTGGGTCTT 1054
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Qy   1055 GGTAAGCT 1114
Db    836 CAGGCAAGCT 895
Qy   1115 ACGAGGA 1174
Db    896 ACGAGGA 955
Qy   1175 TTACGACTTAAA 1234
Db    956 CACGACCTGAA 1015
Qy   1235 TTGAGTGG 1294
Db   1016 TTCTCCGG 1075
Qy   1295 TTAACTAT 1354
Db   1076 TTCACCGAT 1135
Qy   1355 CCAATGAGCAT 1414
Db   1136 CCACCGAT 1195
Qy   1415 GCAGAACACTAA 1474
Db   1196 TGATCGAGAAG 1255
Qy   1475 CCAACTCAGAAGT 1518
Db   1256 CGAGAAGT 1299
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RESULT 3
US-09-023-339-3
; Sequence 3, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
;   APPLICANT: Sutliff, Thomas D.
;   APPLICANT: Rodriguez, Raymond L.
;   TITLE OF INVENTION: Production of `1-Antitrypsin
;   TITLE OF INVENTION: in Plants

```
Db   ||||||  || ||||||| ||||||||  ||||| |||||  ||  || |||
 481 GTCGAGAAGGGGACCCAGGCAAGATCGTGGACCTGGTCAAGGAATTGGCAGGGACACC        540

Qy   ||||||| || ||||||  ||||||||||| || ||| ||||||||||
 876 GTCTTCGCACTAGTTAACTATATATTTTTCAAGGTAAGTGGGAACGTCCTTTCGAGGTT        935

Db   ||||||| || ||||| ||||| || ||||||||||||| ||||||||||
 541 GTCTTCGCCGTCGTCAACTACATCTTCTTCAAGGGCAAGTGGGAGCGCCCGTTCGAGGTG        600

Qy   ||||||| | ||||||  ||| ||||| |||| || ||| ||||||||||
 936 AAAGATACTGAAGAGAGGAAGATTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG        995

Db   |||||| | |||||| ||| ||  |  |||| || |||
 601 AAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACCGTCAAGGTCCCGATG        660

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 996 ATGAAAAGACTGGGTATGTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA       1055

Db   ||||  || ||  || |||| || ||||||||||| || ||||
 661 ATGAAGAGGGCTGGCATGTTCAACATCCAGCACTGCAAGAAGCTCTCCAGCTGGGTGCTC        720

Qy   |||| |||||  ||||| ||||| |||  |||||||||| |||||
1056 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAAGGTAAGCTT       1115

Db   |  |||||||| | ||||| |  ||||| ||||||||||| || |||||
 721 CTCATGAAGTACCTGGGGAACGCCACCGCCATCTTCTTCCTGCCGGACGAGGCAAGCTC        780

Qy   ||||||||| |||||| ||||| ||||||||||||| |||||| |||||||||
1116 CAACATTTAGAGAATGAGTGACTCGACGATTATTACATTATTTAGAGAACGAGGAT       1175

Db   || || || ||||| |||||| | |||| || ||||||||||||||
 781 CAGCACCTGGAGAACGAGCTGACGACGACATCACGGAGTTCCTGGAGAACGAGGAC        840

Qy   |||| ||||||| ||||  |||||| |||||||| ||| ||| ||||
1176 CGTCGTAGCGCTTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA       1235

Db   | ||| | ||| ||||| ||||||||||  || |||||| ||| ||||||
 841 AGGCGGCTCCGCTAGCCTCCACCTCCCGAAGCTGAGCATCACCGGCACGTACGACCTGAAG        900

Qy   || ||||| ||||||||| |||||||  ||||| || ||||||||
1236 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTAACGTGTCCGATTTGAGTGGT       1295

Db   | | ||||| ||||||| |  ||||||| ||||||||||
 901 AGCCTGCTGGGCCAGCTGGGCATCACGAAGTCTTCAGCAACGGCGCGGACCTCGTCCGGC        960

Qy   |||||||||||| ||||||| ||||||| |||| |||||||||||
1296 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT       1355

Db   || |  ||| | ||| || ||||  ||||||||||
 961 GTGACGGAGGAGGGCCCCCTGAAGCTCTCCAAGGCCGTGCTCACGATC       1020

Qy   ||||||  |||||| ||||||| | ||||||| |||||||||| |||
1356 GATGAAAAGGTACCGAGGCCGCCGCCTATCGTTCCTGGAAGCTATTCCAATGAGCAGT       1415

Db   || |  ||||||||||||| |||| || ||||| |  || |||
1021 GACGAGAAGGGGACGGAAGCTGCCGGGCCATCCCCATGTCCATC       1080

Qy   ||||||| ||||||| ||||||||||||||| |  |||| ||||||
1416 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA       1475

Db   ||| ||||||||| ||||||||||||||| ||  |||||||||||
1081 CCGGCCCGAGGTCAAGTTCAACAAGCCCTTCGTTCTCTGATGATCGAGCAGAACACGAAG       1140

Qy   ||||||||||  |||||||| || |||||||||||
1476 AGCCCATTGTTTATGGTAAGGTTGGTCAACCCAACTCAGAAGT       1518

Db   |||||||||||||| ||||||||| |||||||||||
1141 AGCCCCCTCTTCATGGGGAAGGTCGTCAACCCACGCAGAAGT       1183
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RESULT 4
US-09-023-173-5
; Sequence 5, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized RAmy3D signal-mature AAT
US-09-023-173-5

Query Match   41.3%;   Score 629.4;   DB 3;   Length 1260;
Best Local Similarity 70.8%;   Pred. No. 2.3e-153;
Matches 837;   Conservative   0;   Mismatches 346;   Indels   0;   Gaps   0;

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Qy   ||||||| || || || |||||| || |||| ||||| ||||||||| |||
 336 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGGACCAAGACCAT        395

Db   || |||||| ||||||||||| || ||||||| ||| |||| |||||
  76 GAGAGACCCGCAGGGCGACGCCGCCCGGCCCAGAGAAGACCGACACCAGCACCAGGACCAC        135

Qy   ||| ||| ||||||||||| ||||||  ||||||||||||| || |||||
 396 CCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA        455

Db   ||||||| || ||||||||||||| ||||||| ||||||||||||| ||||
 136 CCGACGTTCAACAAGATCAACCCCGAATTTGGCCGAATTGGCCTTCAGCCTGTACCGCCAG        195

Qy   ||||| ||||| |||||| |||| ||| ||| |||||||||||||||||
 456 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCTGTTCTATTGCCACTGCT        515

Db   |||| || ||||||||||| | |||||||||| || |||||||||||||| ||||
 196 CTCGCGGCACCAGTCCAACTCCACCAACATCTTCTTCAGCCCGGTGAGCATCGCCACCGCC        255

Qy   ||||| |||||||| || || |||||| |  || |||||||| ||||||||| |||
 516 TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACCCACCGAGATTTAGAAGGTTTA        575

Db   ||||| || |||||||| | |||||||| ||||||| ||||| |||||||
 256 TTCGCCATGCTGTCCCTGGGTACCAAGGCGACCACCCAGGATCCTCGAAGGGCTG        315

Qy   ||||| |||| |||||| ||| ||| |||||| |||| ||||||||||
 576 AACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGTTTCAAGAGTTGTTG        635

Db   | ||| ||| ||||||| ||||||| || |||||||||| ||||||
 316 AACTTCAACCTGACGGAGATCCCGGAGGCGCAGATCCACGAGGGCGTTCCAGGAGCTGCTC        375

Qy   ||||||  || |||| |||||| ||| || || ||||||||||| |||
 636 AGAACTTGAATCAACCTGATTCTCAATTAACTGTCAATTAACTACTGTAACGGTTTATTTTG        695

Db   |||||||| | |||| ||||||||||| ||||||||||| |||||||| |||
 376 AGGACGCTCAACCAGCCGACTCCCAGCTCCAGCTTCACCACCGCAACGGCGTCTTCCTG        435

Qy   ||||||  ||||||| ||| |||||| | ||||||||||||| |||||
 696 TCTGAAGGTTTAAAATTGTTGACAAATTCCTGAGACAATTCCTGGAGGACGTGAAGAAACTATATCATAGT        755

Db   ||| || || ||||| |||| |||| || |||||| ||||||  ||| |||
 436 TCCGGAGGGCCTCAGCTCGCTCGATAAGTTCCTGGAGGACGTGAAGAAGCTCTACCACTCC        495

Qy   |||||| |||||| ||||| ||||| |||| ||||||| ||||||
 756 GAGGCTTTACCGTTAATTTTGGTGATACTGAGGAAGTCTGAGGAAGCAAATTAATGATTAT        815

Db   ||||| |||| || |||||||| |||| |||| ||||| || ||
 496 GAGGCGTTCACCGTCAACTTCGGGGACACCGAGGAGATCGTTGACCTGGTTAAAGAATTGAT        555

Qy   |||||||| || ||||||||||| |||| || || |||||||||||
 816 GTTGAGAAGGCACCCAGGGTAAGACGGTAAGATCGTTGACCTTAAAGAATTAGATCTGATACC        875

Db   ||||| |||||| ||||||||||  |||||| ||||||||||| |||||||||||
 556 GTCGAGAAGGGGACCCAGGGCAAGATCGTGGACCTTGGTCAAGGATTGGGACAGGGACACC        615

Qy   ||||| || |||| |||||||| ||| ||| || ||||| |||||||||
 876 GTCTTCGCACTAGTTAACTATATATTTTTCATGTTGATCAAGTTCTTCAAGTTCCAATG        935

Db   |||||| || |||| ||||||| || || |||||| ||| || |||||||
 616 GTCTTCGCCGTCGTCAACTACATCTTCTTCAAGGGCAAGTGGGAGCGCCCGTTCGAGGTG        675

Qy   ||||  ||||| || ||||||||  || || |||  |||||| ||||||
 936 AAAGATACTGAAGAGAGGAAGATTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG        995

Db   |||| |  |||||| ||| |||| || ||||  ||||||||| |||||
 676 AAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACCGTCAAGGTCCCGATG        735

Qy   |||| |  |||  || |||||| ||| || ||||||  || |||||||||
 996 ATGAAAAGACTGGGTATGTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA       1055

Db   |||| || || ||| ||||||| ||| ||  ||||||||| |||| ||||||
 736 ATGAAGAGGGCTGGCATGTTCAACATCCAGCACTGCAAGAAGCTCTCCAGCTGGGTGCTC        795
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Qy    478 CTAACATTTTTTTAGTCGTCGTTCTCGTTCTCATTGCCACTGTTGAGTTTGAGGTA  537
Db   1527 CCAATATCTTCTTCTCCCAGTGAGCATCGCTACAGCCGTTGCAATGCTCTCCCTGGGGA 1586

Qy    538 CTAAAGCCGGATACCCATGCAGTTTAGAGAGGTTTAAATTTAATTGACCGAAATCC  597
Db   1587 CCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTC 1646

Qy    598 CAGAAGCCCAAATTCACGAGGTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATT  657
Db   1647 CGGAGGCTGCAGTCCATGCCATGAGAGGCTTCCAGGAACTCCTCGTACCCAGACA 1706

Qy    658 CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTGTCTGAAGGTTAAAATTGGTTG  717
Db   1707 GCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCGTAGTGG 1766

Qy    718 ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTG  777
Db   1767 ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTCAACTTCG 1826

Qy    778 GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA  837
Db   1827 GGGACACCGAAGAGCCAAGAAACAGATCAACGATTACGTGAGGAGGGTACTCAAGGGA 1886

Qy    838 AGATCGTTGACCAGTTAAAGATTAGACTGTGATACCGTCTTCGCCACTAGTTAACTATA  897
Db   1887 AAATTGTGGATTTGGTCAAGGACGTTCGCTCTGGTGAATTACA 1946

Qy    898 TTTTTTCAAGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATT  957
Db   1947 TCTTCTTTAAAGCAAATGGGAGAGCACCCTTTGAAGTCAAGGACACCGACGAAGAGGACT 2006

Qy    958 TTCATGTTGATCAAGTTACTACTGTCAAGTTCCAATGATGAAAAGACTGGGTATGTTCA 1017
Db   2007 TCCAAGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGGCGTTTAGGCATGTTTA 2066

Qy   1018 ATATTCAACATTGCAAAAAATTAAGTCTTGGGTCTTATTAAGTAGTATTTAGGTAACG 1077
Db   2067 ACATCCAGCACTGTGTAAGAAGCTGTCCAGCTGGGTGCCGTGATGAAATACCTGGGCAATG 2126

Qy   1078 CTACTGCTATTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137
Db   2127 CCACCGGCCATCTTCTTCCTGCCGACGAGGGCAAGCTCCAGCACCTGGAAAATGAACTCA 2186

Qy   1138 CTCATGACATTATTACCAAAATTTTAGAGAACGAGGATCGTGCTGCGTCGTCGTCACC 1197
Db   2187 CCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTCGCCAGCTTACATT 2246

Qy   1198 TGCCAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGCCAGTTAGGTA 1257
Db   2247 TACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTTCCTGGGTCAACTGGGCA 2306

Qy   1258 TTACCAAAGTTTTTTCTAACGGTCCGATTTGAGTGGTTACTGAAGAAGCTCCATTAA 1317
Db   2307 TCACTAAGGTCTTCAGCAATGGGCGCTCGACCCTCTGCGGGGTCGACCTGCTGAGCTG 2366

Qy   1318 AATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGAAAAGGTACCGAGGCCG 1377
Db   2367 AGCTCTCCAAGGCCGTCATAAGGCCGTCTCGACGAGAAGAGGGACTGAAGCTG 2426

Qy   1378 CCGGCGCTATGTCCTGGAAGCTATTCCAATGAGCATTCCACCAGAGTTAAATTTAATA 1437
Db   2427 CTGGGGCCGTAGTGTTTTTAGAGCCACTGGTCTATCCCCCGGAGGTCAAGTTCCAACA 2486

Qy   1438 AACCATTCGTTTTTCTGATGATCGAGACACTAAAACTAAAATTACTC 1497
Db   2487 AACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAG 2546

Qy   1498 TTGTCAACCCAACTCAGAAGTA 1519
Db   2547 TGGTGAATCCCACCCCAAAAATA 2568
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Qy   1056 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAAGGTAAGCTT 1115
Db    796 CTCATGAAGTACCTGGGAACGGCCACCGCCATCTTCTTCCTGCCGACGAGGGCAAGCTC 855

Qy   1116 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACCAAAATTTTAGAGAACGAGGAT 1175
Db    856 CAGCACCTGGAGAACGAGCTGACGCACGACATCATCACGAAGTCCTGGAGAACGAGGAC 915

Qy   1176 CGTCGTAGCGCTTCTCGCCACCTGCCAAAGTAAGTACATCACCGGTACTACGACTTAAAA 1235
Db    916 AGGGGCTCCGCTACCTCCACCTCCACCTCCGAGCATCACCGGCACGTACGACCTGAAG 975

Qy   1236 TCTGTTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGGTCCGATTTGAGTGGT 1295
Db    976 AGCCTGCTGGGCCAGTCCAGCTGGGCATCACGAAGGCTTCAGCAAGCCGCCGGACCTCTCCGGC 1035

Qy   1296 GTTACTGAAGAAGCTCCATTAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1355
Db   1036 GTGACGGAGGAGGCCCCCGAAGCTCTCCACCAAGCTGCTCCACGATC 1095

Qy   1356 GATGAAAAGGTACCGAGGCCGCCGGCGCTATGTCCTGGAAGCTATTCCAATGAGCATT 1415
Db   1096 GACGAGAAGGGACGAAGCTGCCGGGCCATGTTCCTGGAGGCCATCCCCATGTCCATC 1155

Qy   1416 CCACCAGAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGACAGAACACTAAA 1475
Db   1156 CCGCCCGAGGTCAAGTTCAACAGACCCTTCGTCTTCCTGATGATCGAGCAGAACACGAAG 1215

Qy   1476 AGCCCATTGTTGTTATGGGTAAGGTCGTCAACCCAACTCAGAAGT 1518
Db   1216 AGCCCCTTCGTCATGGGGAAGGTCGTCAACCCCACGCAGAAGT 1258
```

RESULT 5
US-09-299-141-4
; Sequence 4, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
US-09-299-141-4
; SEQ ID NO 4
; LENGTH: 5932
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT
US-09-299-141-4

Query Match   28.4%;   Score 433.2; DB 4;   Length 5932;
Best Local Similarity   59.7%;   Pred. No 1.7e-102;
Matches   729;   Conservative   0;   Mismatches 493;   Indels   0;   Gaps   0;

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Qy    298 TGTCTGGTAAGTCCGTGTTCCCAGTCAAGGCCATGGAAGACCCTCAAGGCGACGCCG 357
Db   1347 TGGCAGGCCGTGTGCTGCTGGTCCTGTCCTGTCGTGCTGCTGGGCGAGGAGATGCTG 1406

Qy    358 CTCAAAAACCGACCAGCAGTCATCACGACCAAGACCATCCGACCTTTAATAAAATTACTC 417
Db   1407 CCCAGAAGACAGATACATCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 1466

Qy    418 CAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAAATTAGCTCATCAAAGTAATTCTA 477
Db   1467 CCAACCTGGCTGGCTGAGTTCGCCTTCAGCCTATACCGGCCACCAGCGTCCACCACAGCA 1526
```

RESULT 6
US-09-299-141-8
; Sequence 8, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6142
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43msENC-AT
US-09-299-141-8

Query Match   28.4%; Score 433.2; DB 4; Length 6142;
Best Local Similarity 59.7%; Pred. No. 1.7e-102;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

[sequence alignment data]

RESULT 7
US-09-299-141-1
; Sequence 1, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID C-AT
US-09-299-141-1

Query Match   28.4%; Score 433.2; DB 4; Length 6565;
Best Local Similarity 59.7%; Pred. No. 1.7e-102;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

[sequence alignment data]

Db 1986 CTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCGAGTCAAGTTCAACA 2045

Qy 1438 AACCATTCGTTTTTCTGATGATGCGAGCAGACAACTAAAAGCCCATTGTTTATGGTAAGG 1497
           ||| || ||| |||| | ||| | || ||| | |||||| ||||| ||||| |
Db 2046 AACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTTCATGGGAAAAG 2105

Qy 1498 TTGTCAACCCAACTCAGAAGTA 1519

Db 2106 TGGTGAATCCCGCACCCAAAATA 2127

RESULT 8
US-09-299-141-6
; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 6714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43CB-AT
US-09-299-141-6

Query Match   28.4%; Score 433.2; DB 4; Length 6714;
Best Local Similarity   59.7%; Pred. No. 1.7e-102;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

Qy   298 TGTGTGGTAAGTCCTGTGTTCCCCAGTCAAGGCCATGGAAGACCCTCAAGGCGCACGCCG 357
          | || |||||| || || | || || || ||| ||||| ||| |||| ||||
Db 2129 TGGCAGGCCGTGTGCCTGGTCCCTCGGCTGAGGATCCCCCAGGGAGATGCTG 2188

Qy   358 CTCAAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTTAATAAAATTACTC 417
          ||| | | || | ||| | | |||| ||| | | || || || | ||| |
Db 2189 CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 2248

Qy   418 CAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAATAGCTCATCAAAGTAATTCTA 477
          | || | || || || || || | ||| || | ||| ||| |||||||| ||
Db 2249 CCAACCTGGCTGAGTTCGGCTTCGGCCATACCGGCCATACCGGCCGCGCGCCAGTCCAACAGCA 2308

Qy   478 CTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTTCGCCACTGTTGGTA 537
          | |||||| || |||| || ||| || || | | || | || || |||
Db 2309 CCAATATCTTCTTCTCCCCCAGTGAGCATCGGTCTACAGCTTTGCAATGCTCTCCCCGGGA 2368

Qy   538 CTAAAGCCGATACCCATGACGAGATTTTAGAGGTTAAAGATACTGAAGAGGAAGATT 597
          || || | | | ||| || | | |||| ||||| | | || ||| ||
Db 2369 CCAAGGCTGACACTGACCTTCGGTAGCGCTTTCTCTGCACC 2428

Qy   598 CAGAAGCCCAAATTCACGAGGGTTTTCAAGACTTTGAACCTTAATGAAGTAAGG 657
          | || | || ||| | || | || || ||| | || | ||| | | ||
Db 2429 CGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCGGGTCAACCAGCAGACA 2488

Qy   658 CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTGTCGAAGGTTTAAAATTGGTTG 717
          || ||| | ||| ||| || || | | | ||| | || || | | | || ||
Db 2489 GCCAGCTCCAGGCCGTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGCGTGAAGCTGG 2548

Qy   718 ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGACCACTCAGAAGCCTTCAACTTG 777
          || ||| | | || || | || || ||| || | | |||| | || || | ||
Db 2549 ATAAGTTTTTGGAGGATGTTAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCG 2608

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Db   906 TGGCAGGCCGTGTGCCTGGTCCCTCGGCTGAGGATCCCCCAGGGAGATGCTG 965

Qy   358 CTCAAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTTAATAAAATTACTC 417

Db   966 CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 1025

Qy   418 CAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAATAGCTCATCAAAGTAATTCTA 477

Db 1026 CCAACCTGGCTGAGTTCGGCTTCGGCCATACCGGCCGCGCGCCAGTCCAACAGCA 1085

Qy   478 CTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTTCGCCACTGTTGGTA 537

Db 1086 CCAATATCTTCTTCTCCCCCAGTGAGCATCGGTCTACAGCTTTGCAATGCTCTCCCCGGGA 1145

Qy   538 CTAAAGCCGATACCCATGACGAGATTTTAGAGGTTAAAGATACTGAAGAGGAAGATT 597

Db 1146 CCAAGGCTGACACTGACCTTCGGTAGCGCTTTCTCTGCACC 1205

Qy   598 CAGAAGCCCAAATTCACGAGGGTTTTCAAGACTTTGAACCTTAATGAAGTAAGG 657

Db 1206 CGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCGGGTCAACCAGCAGACA 1265

Qy   658 CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTGTCGAAGGTTTAAAATTGGTTG 717

Db 1266 GCCAGCTCCAGGCCGTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGCGTGAAGCTGG 1325

Qy   718 ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGACCACTCAGAAGCCTTCAACTTG 777

Db 1326 ATAAGTTTTTGGAGGATGTTAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCG 1385

Qy   778 GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837

Db 1386 GGGACACCGGAGAGCCAAGAAACAGATCAACAGATTACGTGGAGAAGGGTACTCAAGGGA 1445

Qy   838 AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCCACTAGTTAACTATA 897

Db 1446 AAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACA 1505

Qy   898 TTTTTTTCAAGGTAAGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATT 957

Db 1506 TCTTCTTTAAAGGCAAATGGGAGGAGACCACCGGAGGAAGAGAGACT 1565

Qy   958 TTCATGTTGATCAAGTTACTACTGCTCAAAGTTCCAATGATGAAAAGACTGGGTATGTTCA 1017

Db 1566 TCCACGTGGACCAGGTGACCACCGGCCTATGAAGAGCGTTTAGGCATGTTTA 1625

Qy 1018 ATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTATTAATGAAGTATTTAGGTAACG 1077

Db 1626 ACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTGATGAAATAACCTGGGCAATG 1685

Qy 1078 CTACTGCTATTTTTTTTACCAGAGACGAAGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137

Db 1686 CCACCGACCATCTTCTTCCTGCCTATGAGGGGAAACTACAGCACCTGGAAAATGAACTCA 1745

Qy 1138 CTCATGACACTATTACTACCAAGTTCCTGGAAGGTCTGCCAGCTTACATT 1197

Db 1746 TACCCAAACTGTCCATTACTGGAACCTATGATCTGGAGAGCGTCCTGGGTCAACCTGGGCA 1805

Qy 1198 TGCCAAAGTTAAGTACACCGGTACTATCACCGTCTTAGTTGTTTAGGCCAGTTAGGTA 1257

Db 1806 TACCCAAACTGTCCATTACTGGAACCTATGATCTGGAACTCGAGAGCGTCCATTATT 1865

Qy 1258 TTACCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAGCTCCATTAA 1317

Db 1866 TCACTAAGGTCTTCAGCAAGGCTGACCTCGGGTCACAGAGGAGGCACCCCCTGA 1925

Qy 1318 AATTGAGTAAGCTGTTCACAAAGCCGTCTTAACTATTGATGAAAAGGTACCGAGGCCG 1377

Db 1926 AGTCTCCAAGGCCGTGCATAAGGCGTGTGTGCTGACCACGGCAATGGCCTGTTCCTCAGCGAGGCGTGAAGCTG 1985

Qy 1378 CCGGGCCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACCAGACAGTTAAATTTAATA 1437

Db 2549 ATAAGTTTTTGGAGGATGTTAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCG 2608

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43rmsENC-AT
US-09-299-141-9

Query Match           28.4%;   Score 433.2;   DB 4;   Length 6924;
Best Local Similarity 59.7%;   Pred. No. 1.8e-102;
Matches  729;  Conservative  0;  Mismatches  493;  Indels  0;  Gaps  0;

Qy   298 TGTGTGGTAAGTCCTGTGTTCCCAGTCAGGCCATGGAGACCCTCAAGGCACGGCCG 357
          ||||| |||| || ||  || ||||| || |||||||||  ||||| || ||
Db  2339 TGGCAGGCCTGTGCTGCCTGGTCCCTGTCCTGAGGATCCCCAGGGAGGATGCTG 2398

Qy   358 CTCAAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTTAATAAAATTACTC 417
          ||  |  |  ||| | |||| ||| || || ||  ||   ||  || |||| ||  ||
Db  2399 CCCAGAAGACAGATACATCCCACCATGATCAGTATCAGAGGTCATCAAGATAATCACCC 2458

Qy   418 CAAATTAGCCGAATTGCTTTTCTTTGTGATAGACAATTAGCTCATCAAGTAATTCTA 477
          || || | ||| || |||   | |  | | |||  || |   | ||||    ||| |
Db  2459 CCAACCTGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACCAGTCCAACAGCA 2518

Qy   478 CTAACATTTTTTAGTCCTGTTCTATTGCCACTGCTTCGCCATGTGAGTTTAGGTA 537
          |  || | | | |||  ||   |   |  || || | ||| |   |||| |||
Db  2519 CCAATATCTTCTTCTCCCCAGTGAGCATGTTTGCAATGCTCTCCCCTGGGGA 2578

Qy   538 CTAAAGCCGATACCCATGCAGCGAGATTTTAGAAGTTTAAACTTAATTGACCGAAATCC 597
          |  ||| ||   |  | || |||| | | || |  ||| || || || | | || ||
Db  2579 CCAAGGCTGCACACTCACGATGAAATCCTGGAGGGCCTGAATTCAACCTCACCGGAGATTC 2638

Qy   598 CAGAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTGAAACTTTGAATCAACCTGATT 657
          | |||| | || || ||    |  | ||||  ||  | ||  || || || ||| |
Db  2639 CGGAGGCTCAGATCCATGAAGGCTTCCAGGAAGCTTCCGGAACTCCTCCGGACCA 2698

Qy   658 CTCAATTGCAATTAACTACTGGTAACGTTTATTTGTCTGAAGGTTAAAATTGGTTG 717
          || || ||  | ||  | ||   ||  | | | | |  || || ||  ||  ||
Db  2699 GCCAGCTCCAGTGACCACCGCGTGCCTGAAGTGGCTGAGCGGCCTGAAGCTAGTGG 2758

Qy   718 ACAAATTCCTAGAAGACGTCAAGAAGTCAAAAAGCAAATTAATGATTATGTTGAGAAAGCCACCCAGGGTA 777
          || || || | |||| | || | | |  | | | |||| | ||| || |||| ||| | ||  || |||
Db  2759 ATAAGTTTTTGGAGATGTTAAAAGTTGTACCACTCAGAAGCCTTCACAGAAGACGGGTACTCAGGGA 2818

Qy   778 GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837
          |||| || | ||| || || || ||  | ||  || || ||| |||  | || ||||
Db  2819 GGGACACCGGAGAGAGGCCAAGAAACAGATACGTTGGAGAAGGGGTACTCAAGGGA 2878

Qy   838 AGATCCTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATA 897
          |||| | |||| || ||   |   | || || || | || |  |   |||| |||| ||
Db  2879 AAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACA 2938

Qy   898 TTTTTTTCAAGGGTAAGTCCTGTTCTATTGCCACTGCTTCGCCATGTGAGTTTAGGTA 957
          ||| | | ||| || ||  | |  |  ||  ||| || || || ||  ||| |||
Db  2939 TCTTCTTTAAAGGCAAATGGGAGGAGACCCTTTGAAGTCAAGGACCTTATGATCAGGGACT 2998

Qy   958 TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAGATCGGTATGTTCA 1017
          || || | || || ||  | || | || || |   | | ||||| |||| |  || ||
Db  2999 TCCACGTGGACCAGGTGACCACCCTTTGAACGTCAAGGACCCCTTGAAGTATTAGGTAACG 3058

Qy  1018 ATATTCAACATTGCAAAAATTAAGTTCTTGGGTCTTATTGTGCTGTGATGAAATAACCTGGGCAATG 1077
          | || |  |  ||  ||| | ||| | |  |   | |  ||  | | | | || |  ||||| | |
Db  3059 ACATCCAGCACTGTAAGAAGTCGTGCTATGCCTGTGGTGCTGATGAAATACCTGGGCAATG 3118

Qy  1078 CTACTGCTATTTTTTTTCTACGACCGGTACTTACTGGTGTTTTTAGGCCCAGTTAGGTA 1137
          |  ||| | | | | | ||| |  | || || |  | |  | || |   |||  |||
Db  3119 CCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAATACCACCTGGAAATAGAACTCA 3178

Qy  1138 CTCATGACATTATTACTAAATTTTTAGAGAACGGAGGATCGTCGTAGCGCTTCTCTGCACC 1197
          || || |  | |  || ||| | | | |   || || |  | | | || ||  || |||
Db  3179 CCCACGATATCATCACCAGTTCCTGGAAAATGAAGACAGAGGTCTGCCAGCTTACATT 3238

Qy  1198 TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTGTTAGGCCAGTTAGTA 1257
          || ||| ||| |||| |  ||  || ||   | ||  || |  | | | | || ||||
Db  3239 TACCAAACTGTCCATTACTGGACCTATGATCTGAACCTATGTGTTTAGGCGTCGGTCAACTGGGCA 3298

Qy  1258 TTACCAAAGTTTTTTTCTACGGTGCGATTTGAGTCGTGTTACTGAGAAGAAGCTCCATTAA 1317
          ||||| | | |||  ||    || | |||  | ||    | |  || || || | |  ||
Db  3089 TCACTAAGGTCTTCAGCCATGGGCTGACCTCTCCGGGTCACAGAGGAGGCACCCCTGA 3148

Qy  1318 AATTGAGTAAAGCTGTTCACAAAGCCGTCTTCAACAAGCCGTGCTCTTAACTATTGATGAAAGAAGCGTG 1377
          || || || | || ||  | | | ||  || | |  |  ||   | | || || || | || || ||
Db  3209 AGTCCTCCAAGGCCGCCATAAGGCTGTGCCTGACCTCTGCCTATAAGGGACTGAAGCTG 3208

Qy  1378 CCGGGCTATGTTCCTGGAAGCTATTCCAATGACGATTCCAACGGACTTTCAACA 1437
          ||| ||  | |  || | |  ||  | || | | || | | ||  || | ||||
Db  3269 AACCCTTTGTCTTCTTAATGATTGAACAACAAATACCCAAGTACCAAGTTCCCCCTCTCCCCTGT 3268

Qy  1438 AACCATTCGTTTTCTGATGATCGAGCAGACAGAACACTAAAAGCCCATTGTTTATGGGTAAGG 1497
          | ||| | ||| | |  || || || || || | | || |   || |  || | |  ||||
Db  3209 CTGGGGCCATGTTTTTAGAGGGCCTGAACCAATCCCCCCGGAGCTCAGTTCAAGTTCAACA 3268

Qy  1498 TTGTCAACCCAACTCAGAAGTA 1519
          |||| | |||  || |||||||
Db  3329 TGGTGAATCCCACCCCAAAAATA 3350
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RESULT 9
US-09-299-141-9
; Sequence 9, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 6924
; TYPE: DNA

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Qy  1258 TTACCAAAGTTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA 1317
         | ||| || || ||||| ||  ||| |||| |||  ||||||| || ||||| |||
Db  3299 TCACTAAGGTCTTCAGCAATGGGCGTGACCTCTCCGGGGTCACAGCAGGAGGCACCCCTGA 3358

Qy  1318 AATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGAAAAGGGTACCGAGGCCG 1377
         | ||| |  || |||||||| || |||  || |||||||  || ||||| |||||||| |
Db  3359 AGCTCTCCAAGGCCGTGCATAAGGCTGTCGTGACCATCGACGAGAAAGGGACTGAAGCTG 3418

Qy  1378 CCGGGCCTATGTTCCTGGAAGCTATTCCAATGACCATTCCACCAGAAGTTAAATTTAATA 1437
         | ||| || ||| | |  |||||| || |  ||||||||||||||||| | ||||| |
Db  3419 CTGGGGCCATGTTTTTAGAGGCTGAGGATCCCCAGGAGCTGTCATCCCCCGAGGTCAACA 3478

Qy  1438 AACCATTCGTTTTCTGATGATCGAGCAGAACACTAAAATTACTC 1497
         || ||||| |||| | ||||| |  ||| ||||| || || |
Db  3479 CTGGGGCCATGTTTTTAGAGGGGCCTGAATTTCAACCTCACGGAGATTC 3538

Qy  1498 TTGTCAACCCAACTCAGAAGTA 1519
         || ||||||| || | |||
Db  3539 TGGTGAATCCCACCCAAAAATA 3560
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RESULT 10
US-09-299-141-10
; Sequence 10, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 6924
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43msENCB-AT
US-09-299-141-10

Query Match   28.4%; Score 433.2; DB 4; Length 6924;
Best Local Similarity 59.7%; Pred. No. 1.8e-102;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

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Qy   298 TGTGTGGTAAGTCCGTGTTCCCCAGTCCGTGTCCTGGTCCTGCTGCCTGGTCATTCCCCAGTCCGTGTCCCAGGCGACGCCG 357
         | ||| || ||||| | |||  |||||| ||| ||||||  ||||||||
Db  2339 TGGCAGGCCTGGTGCTGCCTGGTCCTGCCTCCCGGTCCTGCTGCCTGGTCTCCCGAGGGATCCCCAGGAGATGCTG 2398

Qy   358 CTCAAAAACCGACACCAGTCATCACGACCAAGACCATCACCGACTTTTAATAAAATTACTC 417
         || |||| ||  |  ||| |  ||||| ||||| |||| || ||| |||
Db  2399 CCCAGAGACAGAGCAGATACATCCCACCATGATACAGGATCACCACCCACCC 2458

Qy   418 CAAATTTAGCCGCGAATTTGCTTTTCTTTGTATAGACAATTAGCTCATCAAGTAATTCTA 477
         |||||| ||| | ||| || |||| | ||| |  ||  | ||| |  |||| ||| ||
Db  2459 CCAACCTGGCTGAGTTGCGCCTTCAGCCTTTGCAATGCCTTTGCAATGCCCTCGGGGA 2518

Qy   478 CTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCATGTTGAGTTTAGGTA 537
         |||| | |||| || |  |||  | |||   ||| | ||| |||| | ||||| ||
Db  2519 CCAATATCTTCTTCTCCCCAGTGAGCATCGGCTACACAGCCTTTGCAATGCCTCTCCCTGGGGA 2578

Qy   538 CTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTAAACTTTAATTTGACCGAAATCC 597
         || |||||| | |  | || || |||  ||| ||   || ||| |||| ||| |||
Db  2579 CCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACCGGAGATTC 2638

Qy   598 CAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATT 657
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Db  2639 CGGAGGCTCAGATCCATGAAGCTTCCAGGAACGTCCTCCGTACCCTCAACCAGCCAGACA 2698

Qy   658 CTCAATTGCAATTAACTACTGGTAACGTTTATTTTGTCTGAAGGTTAAAATTGGTTG 717
Db  2699 GCCAGCTCCACCGTGACCACCGTGTTCCTCAGCGTGCCTGAAGCTAGTGG 2758

Qy   718 ACAAATTCCTAGAAGACGTCAAGAACTATATCATAGTAGTCGTTTACCGTTAATTTTG 777
Db  2759 ATAAGTTTTGGAGGATGTTAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCG 2818

Qy   778 GTGATACTGAGGAAGCTAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837
Db  2819 GGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCAAGGGA 2878

Qy   838 AGATCGTTGACCAGTTAAAGATTAGATACCGTGATACCGTCTTCGACACTAGTTAACTATA 897
Db  2879 AAATTGTGGATTTGGATTTCAAGGAGCTTGACAGACACAGTTTTGCTCTGTGAATTACA 2938

Qy   898 TTTTTTTCAAGGTAAGTGGGAACGTCCTTTGCAGGTTAAAGATACTCAAGGAAGAGGACT 957
Db  2939 TCTTCTTTAAAGCAAATGGGAGGAGCACCCTTTGAAGTCAAGGACACCGGTATGTTCA 2998

Qy   958 TTCATGTTGATCAAGTTACTACTGTCAAGTTCCAATGATGAAAAGACTCGGTATGTTCA 1017
Db  2999 TCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAGCGTTTAGGCATGTTTA 3058

Qy  1018 ATATTCAACATTGCAAAAAATTAAGTTCTTGGTCTTTATTAATGAAGTATTAGGTAACG 1077
Db  3059 ACATCCAGCACTGTAAGAAGCTGTCCAGCTGGCGTGCTGATGAAATACCTGGCAATG 3118

Qy  1078 CTACTGCTATTTTTTTTTTTTACCAGCAGAAGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137
Db  3119 CCACCGCCATCTTCTTCCCTGCCTGATGAGGGAAACTACAGCACCTGGAAAATGAACTCA 3178

Qy  1138 CTCATGACATTATTACTCATAATTTTTAGAGAACGAGGATCGTCGTAGCGCTTCTCTGCACC 1197
Db  3179 CCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGCCAGCTTACATT 3238

Qy  1198 TGCCAAAGTTAAGTATCACCGGTACTACTTACGACTTAAAATCTGTTTGGCCAGTTAGGTA 1257
Db  3239 TACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCTGAGGTCAACTGGGCA 3298

Qy  1258 TTACCAAAGTTTTTTCTAACGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA 1317
Db  3299 TCACTAAGGTCTTCAGCAATGGGCGTGACCTCTCCGGGGTCACAGCAGGAGGCACCCCTGA 3358

Qy  1318 AATTGAGTAAAGCTGTTCACAAAGCCGTACCGAGGCCG 1377
Db  3359 AGCTCTCCAAGGCCGTGCATAAGGCTGTCGTGACCATCGACGAGAAAGGGACTGAAGCTG 3418

Qy  1378 CCGGGCCTATGTTCCTGGAAGCTATTCCACCAGAAGTTAAATTTAATA 1437
Db  3419 CTGGGGCCATGTTTTTAGAGGCTGAGGATCCCCAGGAGCTGTCATCCCCCGAGGTCAACA 3478

Qy  1438 AACCATTCGTTTTCTGATGATCGAGCAGAACACTAAAAATTACTC 1497
Db  3479 AACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCCTTCTCATGGGAAAAG 3538

Qy  1498 TTGTCAACCCAACTCAGAAGTA 1519
Db  3539 TGGTGAATCCCACCCAAAAATA 3560
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RESULT 11
US-09-299-141-11
; Sequence 11, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL

```
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6924
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43rmsENCB-AT
US-09-299-141-11

Query Match      28.4%;   Score 433.2;  DB 4;   Length 6924;
Best Local Similarity   59.7%;   Pred. No. 1.8e-102;
Matches  729;  Conservative   0;  Mismatches  493;  Indels   0;  Gaps   0;

Qy   298 TGTGTGGTAAGTCCTGTGTTCCCCAGTCAGGCCATGAGAAGACCCTCAAGGCGACGCCG 357
Db  2339 TGGCAGGCCGTGTCGTGCCTGGTCCCTGTCTCCCTGCCTGGAGGATCCCAGGGAGATGCTG 2398
Qy   358 CTCAAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTAATAAAATTACTC 417
Db  2399 CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 2458
Qy   418 CAAATTTAGCCGAATTGCTTTTCTTTGTATAGACAATTAGCTCATCAAAGTAATTCTA 477
Db  2459 CCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCCACCAGTCCAACAGCA 2518
Qy   478 CTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCTTTCGCCATGTGAGTTTAGTTA 537
Db  2519 CCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGA 2578
Qy   538 CTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAACTTTAATTGACCGAAATCC 597
Db  2579 CCAGGGCCGTGTCGACACTCAGCGATGAAATCCTGGAGGCCTGAATTCAACCTCACGGAGATTC 2638
Qy   598 CAGAAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATT 657
Db  2639 CGGAGGCTCAGATCCATGAAGGCTTCAGGAACTCCTCCGTACCCTCAACCAGCCAGACA 2698
Qy   658 CTCAAGTGCAATTAACTACTGGTAACGGTTTATTTTGTCTGAAGGTTTAAAATTGGTTG 717
Db  2699 GCCAGCTCCAGCTGACCACCACCGGCCAATGGCCTGTTCCTCCAGCAGGGGCCTGAGCTAGTGG 2758
Qy   718 ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTACCGTTAATTTTG 777
Db  2759 ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAGCCTTCACTGTCAACTTCG 2818
Qy   778 GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837
Db  2819 GGGACACCGAAGAGGCCAAGAAACAGATCACGATTACCGTGGAAGGGTACTTCAAGGGA 2878
Qy   838 AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGGCACTAGTTAACTATA 897
Db  2879 AAATTGTGGATTTGGTCAAGGAGTTTGACGAGACACAGTTTTTTGCTCTGGTGAATTACA 2938
Qy   898 TTTTTTTCAAGGGTAAGTGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATT 957
Db  2939 TCTTCTTTAAAGCAAATGGCAAATGGGAGAGACCCTTTGAAGTCAAGGAGGAGATGGACT 2998
Qy   958 TTCATGTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAAGACTGGGTATGTTCA 1017
Db  2999 TCCACGTGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGGCGTTTAGGCCATGTTTA 3058
Qy  1018 ATATTCAACATTGCAAAAATTCAAAAAATTAAGTTCTTGGGCTTATTAATGAAGTATTTAGGTAACG 1077
Db  3059 ACATTCCAGCACTGTAAGAGCTGTCCCAGTCGTGCTGCTTCGAGCTGTGCTGATGAAATACCTGGGCAATG 3118

Qy  1078 CTACTGCTCATTTGTTTTTTTTTACCAGACGAAGCTGAAGCTTCAACATTTAGAGAATGAGTTGA 1137
Db  3119 CCACCGCCATCTTCTTCCTGCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAAATGAACTCA 3178
Qy  1138 CTCATGACATTATTACTAACAATTTTTAGAGAACGAGGATCGTCGTAGCGCTTCTCTGCACC 1197
Db  3179 CCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGCCAGCTTACATT 3238
Qy  1198 TGCCAAAGTAAGTAATCACCGGTACTTACGACTTAAAATCTGTTTAGGCCAGTTAGGTA 1257
Db  3239 TACCCAAACTGTCCATTACTGGAACCTATGATCTGGAAGAGCGCTCTGGGTCAACTGGGCA 3298
Qy  1258 TTACCAAAGTTTTTCTAACGGTGCCGATTTGAGTGTGTTACTGAAGAAGCTCCATTAA 1317
Db  3299 TCACTAAGGTCTTCAGCAATGGGCTGACCTTCCCGGGTCACAGAGGAGGCACCCCTGA 3358
Qy  1318 AATTGAGTAAAGCTGTTCACAAAGCCCTCTTAACTATTGATGAAAAGGTACCGAGGCCG 1377
Db  3359 AGCTCTCCAAGGCCGTGCCATAAGGCGTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTG 3418
Qy  1378 CCGGCGCTATGTTCCTGAAGCTATTCCAATGACATTCCACCAGAAGTTAAATTTAATA 1437
Db  3419 CTGGGCGCCATGTTTTTAGAGGCCATACCCATGTCTCATCCCCCCGGAGGTCAAGTTCAACA 3478
Qy  1438 AACCATTCGTTTTCTGATGATCGAGCAGAGACAACTAAAAGCCCATTGTTGTTATGGTAAGG 1497
Db  3479 AACCCTTTGTCTTCTTAATGATTGAACAAAAATACCAAGTCTCCCCTCTTCATGGGAAAAG 3538
Qy  1498 TTGTCAACCCAACTCAGAAGTA 1519
Db  3539 TGGTGAATCCCACCCAAAAATA 3560

RESULT 12
US-09-299-141-7
; Sequence 7, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6981
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID C-AT2
US-09-299-141-7

Query Match      28.4%;   Score 433.2;  DB 4;   Length 6981;
Best Local Similarity   59.7%;   Pred. No. 1.8e-102;
Matches  729;  Conservative   0;  Mismatches  493;  Indels   0;  Gaps   0;

Qy   298 TGTGTGGTAAGTCCTGTGTTCCCCAGTCAGGCCATGAGAAGACCCTCAAGGCGACGCCG 357
Db   127 TGGCAGGCCGTGTCGTGCCTGGTCCCTGTCTCCCTGCCTGGAGGATCCCAGGGAGATGCTG 186
Qy   358 CTCAAAAAACCGACACCAGTCATCACGACCAAGACCATCCGACTTTAATAAAATTACTC 417
Db   187 CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC 246
Qy   418 CAAATTTAGCCGAATTGCTTTTCTTTGTATAGACAATTAGCTCATCAAAGTAATTCTA 477
Db   247 CCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCCACCAGTCCAACAGCA 306
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RESULT 13
US-09-299-141-3
; Sequence 3, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;   APPLICANT: FLOTTE, TERENCE R.
;   APPLICANT: SONG, SIHONG
;   APPLICANT: BYRNE, BARRY J.
;   APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7054
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID dE-AT
US-09-299-141-3

Query Match        28.4%;    Score 433.2; DB 4;  Length 7054;
Best Local Similarity   59.7%;    Pred. No. 1.8e-102;
Matches  729;    Conservative    0;  Mismatches  493;  Indels    0;  Gaps  0;
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Right column alignment:

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Db   1395  TGGCAGGCCTGTGTGCCTGGTCCCTGTCTCCCGGCTGAGGATCCCCAGGGAGGATGCTG      1454

Qy    358  CTCAAAAAACCGACACCAGTCATCGACCAAGACCATCCGACTTTTAATAAAATTACTC        417
                  ||| | | || ||  | ||  ||   | |  |||
Db   1455  CCCGAAGACAGATACATCCCACCACCAGATCAGGATGACATCCAACAAGATCACCC         1514

Qy    418  CAAATTAGCCGAATTGCTTTTCTTTTCTTTGTATAGACAATTAGCTCATCAAAGTAATTCTA    477
                  ||| | ||| ||  |  |   |  ||  || |
Db   1515  CCAACCTGCCTGAGTTCGCCTTCAGCCTATACCGCAGCTGCACACCAGTCCAACAGCA       1574

Qy    478  CTAACATTTTTTTAGTCCTGTGTTCTATTGCCACTGTTGAGTTTAGGTA                 537
                  ||| | | || || |  | |   | |||
Db   1575  CCAATATCTTCTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGA        1634

Qy    538  CTAAAGCCGATACCCATGACGAGATTTAGAAGGTTTAAACTTAATTGACCGAAATCC         597
                  || ||||| || | || |   | ||| |  |  ||
Db   1635  CCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTC      1694

Qy    598  CAGAAGCCCAAATTCACGAGGTTGTTGAGAGTTGTGAAGAACTTTGAATCAACCTGATT       657
                  | ||||| ||| ||| ||  | |  | |  || |||
Db   1695  CGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACA      1754

Qy    658  CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCTCAGCCGAGGCCTTAAAATTGGTTG  717
                  || || ||| ||  |  | | | |  || || | ||
Db   1755  GCCAGCTCCAGCTGACCACCGCAATGGCCTCGTGTTCCTCCAGCGGCCTGAAGCTAGTGG      1814

Qy    718  ACAAATTCCTAGAAGACGTCAAGAAACTATATCGTCTTGAAGAGGAAGATT              777
                  | |||| || || || |   | |  ||| |  |  ||
Db   1815  ATAAGTTTTTGGGAGATGTTAAAAAGTGTACCACTCAGAGAGCTTCACTGTCAACTTCG      1874

Qy    778  GTGATACTGAGGAAGCTAAAAAAGCAAATTAATGATTATGTTGAGAAGCAACCAGGGTA       837
                  | || || ||| | ||||| || || |  |  |  || |
Db   1875  GGGACACCGAAGAGGCCAAGAAACAGATCAACGATCACAGATTACGTGGGAGAAGGGTACTCAAGGGA  1934

Qy    838  AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATA      897
                  ||| | || || || |   | ||   ||| |  | |
Db   1935  AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATA      1994

Qy    898  TTGTCAACCAACTCAGAAGTA                                             957
                  || || || ||  |||| |
Db   1995  TTGGTGAATCCACCCAAAAATA                                            2054
```

Left column alignment:

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Qy    478  CTAACATTTTTTTAGTCCTGTGTTCTATTGCCACTGTTGAGTTTAGGTA                 537
                  || |  | |   | |||   ||  |  ||
Db    307  CCAATATCTTCTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGA        366

Qy    538  CTAAAGCCGATACCCATGACGAGATTTAGAAGGTTTAAACTTAATTGACCGAAATCC         597
                  || ||| | || |  | |   | ||| |  |  ||
Db    367  CCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTC      426

Qy    598  CAGAAGCCCAAATTCACGAGGTTGTTGAGAGTTGTGAAGAACTTTGAATCAACCTGATT       657
                  | ||||| ||| ||| ||  | |  | |  || |||
Db    427  CGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACA      486

Qy    658  CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCTCAGCCGAGGCCTTAAAATTGGTTG  717
                  || || ||| ||  |  | | | |  || || | ||
Db    487  GCCAGCTCCAGCTGACCACCGCAATGGCCTCGTGTTCCTCCAGCGGCCTGAAGCTAGTGG      546

Qy    718  ACAAATTCCTAGAAGACGTCAAGAAACTATATCGTCTTGAAGAGGAAGATT              777
                  | |||| || || || |   | |  ||| |  |  ||
Db    547  ATAAGTTTTTGGGAGATGTTAAAAAGTGTACCACTCAGAGAGCTTCACTGTCAACTTCG      606

Qy    778  GTGATACTGAGGAAGCTAAAAAAGCAAATTAATGATTATGTTGAGAAGCAACCAGGGTA       837
                  | || || ||| | ||||| || || |  |  |  || |
Db    607  GGGACACCGAAGAGGCCAAGAAACAGATCAACGATCACAGATTACGTGGGAGAAGGGTA       666

Qy    838  AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATA      897
                  |||| | ||| || || |  | || | ||| |  |
Db    667  AAATTGTGGATTTGGTCAAGGAAGCTTGACAGAGCTTCCTTTCGAGGTGTCTGGTGAATTACA   726

Qy    898  TTTTTTCAAGGTAAGTGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATT         957
                  ||| || || || | || || || |
Db    727  TCTTCTTAAAGGCAAATGGGAAGACGACCCCTTTGAGTCAAGGACACCGAGGAGGAAGAGGACT 786

Qy    958  TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAGTGCTGGTATGTTCA       1017
                  || | | | |  ||| | | | || |   ||
Db    787  TCCACGTGGACCAGTGACACTGCACCGTGAAGGTGCGTTTAGGTAGTATTAGGCCATGTTTA    846

Qy   1018  ATATTCAACATTGCAAAAAATTAGAGTTCTTGGGTCTTATTAATGAAGTATTTAGGTAACG    1077
                  || ||| ||  || || |  | |   |  | ||  ||
Db    847  ACATTCCAGCACTGTAAGAGCTGAAGCTGTGTCCAGCTGGTGCTGCTGATGAAATAACCTGGGCAATG 906

Qy   1078  CTACTGCTATTTTTTTTTTACCAGGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA        1137
                  | || |  | | || | ||  | | | || |   |
Db    907  CCACCGCCATCTTCTCTCCGCTCGATGAGGGGAAAGAAACTACACCTGGAAAATGAACTCA     966

Qy   1138  CTCATGACATTATTATTACTAAATTTTACTTACACGATCTTCGTAGCGCTTCTCTGCACC     1197
                  || || || ||  | | || | ||  ||  |
Db    967  CCCACGATATCATCACCAGTCCTGGAAAATGAGAGACAGAGGTCTGCCAGCTTACATT        1026

Qy   1198  TGCCAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGTCCAGTTAGGTA     1257
                  || || || || ||| |   | | |  ||
Db   1027  TACCCAAACTGTCCATTACTGGAACCTGAAGACGTCTGGGTCAACTGGGCA              1086

Qy   1258  TTACCAAAGTTTTTTTTTCCTAACGGTGCCGATTTGAGTGTGTTACTGGAGAAGCTCCATTAA  1317
                  || || |  | ||   |  || |  || |  ||
Db   1087  TCACTAAGGTCTTCAGCAATGGGCTGACCCTCTGACGAATATGAGGTCTCGGGGTCAACTGGGCA 1146

Qy   1318  AATTGAGTAAAGCTGTTCACAAGCTGTCTTAAACTATTGATGAAAGAAAGGGTACCGAGGCCG   1377
                  |  || || || || | |  | || | | |
Db   1147  AGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGATGAGCCATGACGAGAAGAGGGACTGAAGCGTG 1206

Qy   1378  CCGGGCCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACCAGAAGTTAAAATTTAATA     1437
                  ||| |  | || |  | ||| | ||  | || |
Db   1207  ATAAGTTTTTGGGAGATGTTAAAATCTGCTATGATCTGAAGCAGTCTTAAATTTAATA       1266

Qy   1438  AACCATTCGTTTTTCTGATGATCGAGCAGAACAACTAAAAGCCCATTGTTTATGGGTAAGG    1497
                  ||| || || |  |  |  |  || | |   |
Db   1267  AACCCTTTGTCTTCTTAATGATTGAACAAAATACACCAAGTCTCCCCTCTTCATTGGGAAAAG   1326

Qy   1498  TTGTCAACCAACTCAGAAGTA                                             1519
                  || || || || || |
Db   1327  TGGTGAATCCCACCCAAAAAATA                                           1348
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Db  1746  TGGCAGGCCGTGTCGTGCTCGGTCCCTGCCTGGCTGCCCTGTCCCTCCCTGGCTGAGGATCCCGAGGGAGGATGCTG  1805

Qy   358  CTCAAAAAACCGACACCAGTCATCACGACAGCCATCCGACTTTAATAAAATTACTC  417
          | ||  || || ||  || || || ||||  || || ||   ||||  || |||
Db  1806  CCCAGAAGACAGATACATCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC  1865

Qy   418  CAAATTTAGCCGAATTGCTTTTCTTGTATAGACAATTAGCTCATCAAAGTAATTCTA  477
          | ||  || || ||   ||  ||  | ||  ||  ||   |||| |  |||
Db  1866  CCAACCTGGCTGAGTTCGCCTTCGGCCTATACCGCCAGTCAACACCAGTCCAACAGCA  1925

Qy   478  CTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCCGCCATGTGAGTTAGGTA  537
          |  | ||  || || || || ||  | ||  || || |  ||  | || ||| |||
Db  1926  CCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGA  1985

Qy   538  CTAAAGCCGATACCCATGCAGAGATTTAGAAGTTAAACTTTAATTTGACCGAAATCC  597
          |  || || || |||| || || ||    || || || || || |  || |||
Db  1986  CCAAGGCTGCACTCACGATGAAATCCTGGAGGGCCGTGAATTCAACCTCACGGAGATTC  2045

Qy   598  CAGAAGCCCAAATTCACGAGGGTTTGCTGGAGTTGTTGAATCAACCTGATT  657
          | || || ||   || || ||    |||  || || ||   |||| ||
Db  2046  CGGAGGCTCAGATGCAATGGCCTTCCTGGGTCAACTGGGCA  2105

Qy   658  CTCAATTGCAATTAACTACTGGTAACGGTTTATTTTGTCTGAAGGTTTAAAATTGGTTG  717
          || || || ||  || || ||  || || | |||  | ||   ||| |||| || ||
Db  2106  GCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGG  2165

Qy   718  ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTG  777
          | ||  || ||  || || || || |  |    || || ||  ||   | |||  |
Db  2166  ATAAGTTTTTGGAGGATGTTAAAAGTGTACCACTCAGAAGCCTTCACTGTCAACTTCG  2225

Qy   778  GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAGATACTGAAGGGTA  837
          |  | || || || || ||  || || || || || |  ||  ||  | ||  ||||
Db  2226  GGGACACCGAGAGGCCAAGAAACGATCAACGATTACGTGGAAGAGGTACTCAAGGGA  2285

Qy   838  AGATCGTTGACCTAGTTGAAGATGTAAGAATTAGATGCGTGATACCGTCTTCCCACTAGTTAACTATA  897
          | || || ||  || || || ||  || ||  || | ||  | || ||  |  || || ||
Db  2286  AAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTGTCTCGTGGTGAATTACA  2345

Qy   898  TTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGGAAGATT  957
          |     ||||  || || || ||  || |  || || || ||    || || || | |
Db  2346  TCTTCTTTAAAGGCAAATGGGACGACCCTTTGAGTCAGAAGCAAGGACACCGAGGAGGACT  2405

Qy   958  TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAAGTGATGAAAAGACTGGGTATGTTCA  1017
          ||  | ||  ||  ||  || || ||  | ||  || |  | |||  || || |||  |
Db  2406  TCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGAGCGTTTAGGCATGTTTA  2465

Qy  1018  ATATTCAACATTGCAAAAATTAAGTTCTTGGGTCTTATTGTATAATGAAGTATTAGGTAACG  1077
          | ||||| |||   ||  ||| ||   |  || |||  | ||  | || || ||  ||
Db  2466  ACATCCAGCACTGTAAGAGCTGGTCGTGCTGCTGTGTCTGATGAAATACCTGGGCAATG  2525

Qy  1078  CTACTGCTATTTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA  1137
          |  | || |||  ||    || || ||  || || ||| ||   | ||  || || |||
Db  2526  CCACCGCCATCTTCTTTCCGCCTGATGAGGGGAAACTACAGCCACCTGGAAAATGAACTCA  2585

Qy  1138  CTCATGACATTATTACTAAATTTTTAGAGAACCAGGAATCGTCGTAGCCGTTCTCTGCACC  1197
          || ||  | || || || ||   ||    || || ||   |  | ||  |  |  ||||
Db  2586  CCCAGTATCATCACCAAGTTCCTGGAAAATGAAGCGTCTGCCAGCTTACATT  2645

Qy  1198  TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTAGGCCAGTTAGGTA  1257
          || || || || || || ||||  |  || |||   | || ||  || ||  || |||
Db  2646  TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTAGGCCAGTAGGTA  2705

Qy  1258  TTACCAAAGTTTTTCTACAGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA  1317
          ||   || ||     | || ||   |  |  || ||    || || || || || |
Db  2706  TCACTAAGGTCTTCAGCAATGGGCTGACCCTCTCCGGGGTCGACCCTGACCCTGA  2765

Qy  1318  TACCAAAGTTTTTCTACAGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA  1377
          || || || ||   | || ||   |  |  || ||    || || || || || |
Db  2766  AGCTCCAAGGCCGTATCAAGGCTGTAAGGCCTATTCCAATGAGCATTCCACCAGAGTCG  2825

Qy  1378  TTACCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA  1437
          || || || ||     || || ||   |  |  || ||    || || ||
Db  2826  CTGGGCCCATGTTTTTGAGAGGCCATGTTTTTGAGAGGGACGGACGCGCCG  2885
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Qy   958  TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATGATGAAAAGACTGGGTATGTTCA  1017

Db  2055  TCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGAGCGTTTAGGCATGTTTA  2114

Qy  1018  ATATTCAACATTGCAAAAATTAAGTTCTTGGGTCTTATTGTATAATGAAGTATTAGGTAACG  1077

Db  2115  ACATCCAGCACTGTAAGAGCTGGTCGTGCTGTGTCTGATGAAATACCTGGGCAATG  2174

Qy  1078  CTACTGCTATTTTTTTTTTTACCAGACGAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA  1137

Db  2175  CCACCGCCATCTTCTTCTCCGCCTGATGAGGGGAAACTACAGCCACCTGGAAAATGAACTCA  2234

Qy  1138  CTCATGACATTATTACTAAATTTTTAGAGAACCAGGAATCGTCGTAGCCGTTCTCTGCACC  1197

Db  2235  CCCAGTATCATCACCAAGTTCCTGGAAAATGAAGCGTCTGCCAGCTTACATT  2294

Qy  1198  TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTAGGCCAGTTAGGTA  1257

Db  2295  TACCCAAACTGTCCATTACTGGCCATTACCGCCAGTGATCTCATCCCCGAGAGCTCGGGCA  2354

Qy  1258  TTACCAAAGTTTTTCTACAGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA  1317

Db  2355  TCACTAAGGTCTTCAGCAATGGGCTGACCCTCTCCGGGGTCGACCCTGACCCTGA  2414

Qy  1318  AATTGAGTAAAGCTGTTCACAAAGCCGTCATAAGCCGTCTTAACTATTGATGAAAAGGTACCGAGGCCG  1377

Db  2415  AGCTCCAAGGCCGTATCAAGGCTGTAAGGCCTATTCCAATGAGCATTCCACCAGAGTCG  2474

Qy  1378  CCGGGCTATGTTCCTGGAGCTATTCCAATGAGCATTCCAATGATGAAGAAGTAAAATTTAATA  1437

Db  2475  CTGGGCCCATGTTTTTGAGAGGCCATGTTTTTGAGAGGGACGGACGCGCCG  2534

Qy  1438  AACCATTCGTTTTCTGATGATCGAGCAGACACTAAAAGCCCATTGTTTATGGGTAAGG  1497

Db  2535  AACCCTTTGTCTTCTTAATGATTGAACAAAATACCAGGTCTCCCTCTTCATGGGAAAAG  2594

Qy  1498  TTGTCAACCAACTCAGAAGTA  1519

Db  2595  TGGTGAATCCCACCCCAAAAATA  2616
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RESULT 14
US-09-299-141-2
; Sequence 2, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID E-AT
US-09-299-141-2

Query Match 28.4%; Score 433.2; DB 4; Length 7405;
Best Local Similarity 59.7%; Pred. No. 1.8e-102;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

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Qy   298  TGTGTGGTAAGTCCGTGTTCCCAGTCAAGGCCATGGAAGACCCTCAAGGCGACGCCG  357
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Db  2826  CTGGGCCCATGTTTTTGAGAGGCCATGTTTTTGAGAGGGACGGACGCGCCG
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Db   181 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAGAAATCCTGAGGGGCTG 240

Qy   576 AACTTTAATTTGACCGAAATCCCAGAGAGCCCAAATCACGAGGGTTTTCAAGAGTTGTTG 635
Db   241 AATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCTTCAAGAGGCTTCAGGAACTCCTC 300

Qy   636 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 695
Db   301 CGTACCCTCAACCAGCCAGCACCAGCTCCAGCTGACAGCTCCAGCCAATGGCCTGTTCCTC 360

Qy   696 TCTGAAGGTTAAAATTGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 755
Db   361 AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 420

Qy   756 GAGGCTTTTACCGTTAATTTTGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 815
Db   421 GAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTAC 480

Qy   816 GTTGAGAAAGGCACCCAGGGTAAGACGTGTGACCTAGTTGAAAGAATTAGAATCGTGATACC 875
Db   481 GTGGAGAGGGGTACTCAAGGGGAAAATTGTGGATTTGGTCAACGAGCTTGACAGAGACACA 540

Qy   876 GTCTTCGCCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT 935
Db   541 GTTTTTGCTCTGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTC 600

Qy   936 AAAGATACTGAAGAGGAAGATTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG 995
Db   601 AAGGACACCGAGGAAGAGGACTTCCACGTGACCAGGTGACCACCGTGAAGGTGCCTATG 660

Qy   996 ATGAAAAGACTCGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGTCTTA 1055
Db   661 ATGAAGCCTTTAGGCATGTTAACATCCAGCACTGTAAGAGCTGTCAGCTGGGTGCTG 720

Qy  1056 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTTACCAGACGAAGGTAAGCTT 1115
Db   721 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTA 780

Qy  1116 CAACATTTAGAGAATGAGTTGACTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGAT 1175
Db   781 CAGCACCTGGAAAATGAACTCACCCCACGATATCACCAAGTTCCTGGAAAATGAAGAC 840

Qy  1176 CGTCGTAGCGCTTCTCTGCCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 1235
Db   841 AGAAGGTCTGCCCAGCTTACATTTACCCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGT 900

Qy  1236 TCTGTTTAGGCCAGTTAGGTATTACCAAAGTTTTCTACAACGGTCCGATTTGAGTGGT 1295
Db   901 AGCGTCCTCGGGTCAACTGGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGG 960

Qy  1296 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGTTGTTCACAAAGCCGTCTTAACTATT 1355
Db   961 GTCACAGAGAGGAGGCACCCCGTGAAGCTCTCCAAGGCCGTGCATAAGGCGTGTGCTGACCATC 1020

Qy  1356 GATGAAAAGGGTACCGAGGCGCCGCCGTATGTTCCTGTTTCCTATTGCCAAGCTATT 1415
Db  1021 GACGAGAAAGGGACTGAGCGCGCCGGCCATGCTTTTTTAGAGGCCCATACCCATGTCTATC 1080

Qy  1416 CCACCAGAAGTTAATTTAATAAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1475
Db  1081 CCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAG 1140

Qy  1476 AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAAGTA 1519
Db  1141 TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATA 1184
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Qy  1438 AACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAAAAGCCCATTGTTTATGGGTAAGG 1497
Db  2886 AACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAG 2945

Qy  1498 TTGTCAACCCAACTCAGAAGTA 1519
Db  2946 TGGTGAATCCCACCCAAAAATA 2967
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RESULT 15
US-09-023-339-2
; Sequence 2, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
;   APPLICANT: Sutliff, Thomas D.
;   APPLICANT: Rodriguez, Raymond L.
;   TITLE OF INVENTION: Production of '1-Antitrypsin
;   TITLE OF INVENTION: in Plants
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: P.O. Box 60850
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/023,339
;   FILING DATE: 13-FEB-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/037,991
;   FILING DATE: 13-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Petithory, Joanne R
;   REGISTRATION NUMBER: P42,995
;   REFERENCE/DOCKET NUMBER: 0665-0003.30
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-324-0880
;   TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1185 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   CLONE: native AAT coding sequence
US-09-023-339-2

Query Match   28.2%; Score 430.4; DB 3; Length 1185;
Best Local Similarity 60.2%; Pred. No. 5.3e-102;
Matches 713; Conservative 0; Mismatches 471; Indels 0; Gaps 0;

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Qy  336 GAAGACCCTCAAGGCGACGCCGCCTCAAAAAACCGACCAGTCATCACGACCAAGACCAT 395
Db    1 GAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATCATCCACCATGACATCAGGATCAC 60

Qy  396 CCGACTTTTAATAAATTACTCCAAATTTAGCCACGGCGAATTTGCTTTTCTTTCTTGTATAGACAA 455
Db   61 CCAACCTTCAACAAGATCACCCCCAACCTGCCGAGTTCGCCTTCAGCCTTATACCGCCAG 120

Qy  456 TTAGCTCATCAAAGTAAATTCTACTAACATTTTTTTTTAGTCCTGTTTCTATTGCCCACTGCT 515
Db  121 CTGGCACCACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGCATCGCTACAGCC 180

Qy  516 TTCGCCATGTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA 575
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Search completed: December 6, 2002, 23:35:07
Job time : 86 secs